

# Detection of *Shigella* Outbreaks in Argentina using WHONET and SaTScan

John Stelling, M.D., M.P.H.<sup>1</sup>, Katherine Yih, Ph.D., M.P.H.<sup>2</sup>, Marcelo Galas<sup>3</sup>, Martín Kulldorff, Ph.D.<sup>2</sup>, Mariana Pichel, Ph.D.<sup>3</sup>, Raquel Terragno<sup>3</sup>, Ezequiel Tuduri<sup>3</sup>, Salomé Espetxe<sup>4</sup>, Norma Binsztein<sup>3</sup>, Thomas F. O'Brien, M.D.<sup>1</sup>, Richard Platt, M.D., M.S.<sup>2</sup>, and Collaborative Group WHONET-Argentina

<sup>1</sup>Brigham and Women's Hospital, <sup>2</sup>Harvard Pilgrim Health Care, Harvard Medical School, <sup>3</sup>Departamento Bacteriología, Instituto Nacional de Enfermedades Infecciosas ANLIS "Dr. C. Malbrán", <sup>4</sup>Dirección Epidemiología, Ministerio de Salud, Argentina

## OBJECTIVE

This paper describes the application of the WHONET software integrated with SaTScan to the detection of *Shigella* outbreaks in a national database using a space-time cluster detection algorithm in simulated real-time and comparison of findings to outbreaks reported to the Ministry of Health (MOH).

## BACKGROUND

Electronic laboratory-based surveillance can significantly improve the diagnostic specificity and response time of traditional infectious disease surveillance. Under the project "Models of Infectious Disease Agent Study" (MIDAS), we wished to evaluate the application of space-time outbreak detection algorithms utilizing SaTScan [1] to a national database of routinely collected microbiology laboratory data.

The Collaborative Group WHONET-Argentina, established in 1986, comprises 70 microbiology laboratories nationwide [2], all of which enter their data into the widely used WHONET 5.4, a free software developed by our group and distributed through the World Health Organization to over 90 countries.

## METHODS

We applied Kulldorff's space-time permutation scan method to WHONET-Argentina data to look for clusters of *Shigella* spp. from July 2006 through June 2007, simulating prospective surveillance. We searched for clusters on the basis of genus, species, and antimicrobial resistance phenotype in separate analyses, using one year of historical data and a 30-day scanning window. Data analysis was performed using an adapted version of the WHONET 5.4 software into which SaTScan features were integrated. WHONET executes SaTScan in batch mode, and then integrates findings into the WHONET display, as in Figure 1.

## RESULTS

There were 2,041 isolates of *Shigella* spp. analyzed in the twelve-month period during which six outbreaks were reported to the MOH. We identified

19 statistical "events", depicted in Figure 2, of which 3 overlapped in space and time with known outbreaks and 2 additional ones may have corresponded with known outbreaks, relationships supported by available serotyping and PFGE results. Of the 14 remaining events, several may have represented true outbreaks not reported to the MOH. The most discriminating analyses were those involving resistance phenotypes.

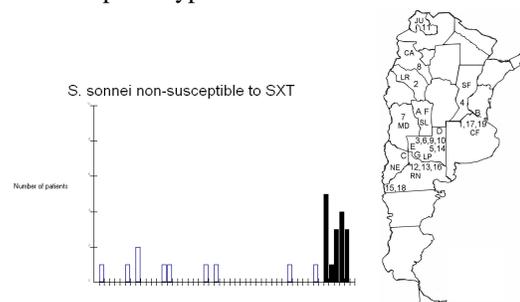


Figure 1

Figure 2

Figure 1 – Weekly distribution of *S. sonnei* isolates non-susceptible to SXT for a laboratory in La Pampa. Event 5 is indicated in solid bars.

Figure 2 – 6 outbreaks reported to the Ministry of Health and 19 statistical "events" detected by SaTScan, July 2006-June 2007.

## CONCLUSIONS

The prospects for integrating advanced statistical methods with existing national laboratory-based surveillance strategies for outbreak detection seem excellent. The integration of WHONET and SaTScan permits the expansion worldwide of advanced statistical techniques for the detection of outbreaks.

## REFERENCES

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Further Information:  
John Stelling, [jstelling@rics.bwh.harvard.edu](mailto:jstelling@rics.bwh.harvard.edu)  
[www.who.int/drugresistance/whonetsoftware](http://www.who.int/drugresistance/whonetsoftware)